Bowman, A.
10/605498

FILE 'REGISTRY' ENTERED AT 15:43:15 ON 15 DEC 2005
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STRUCTURE FILE UPDATES: 14 DEC 2005 HIGHEST RN 869939-98-0
DICTIONARY FILE UPDATES: 14 DEC 2005 HIGHEST RN 869939-98-0

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

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* *
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
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http://www.cas.org/ONLINE/UG/regprops.html

L1 29 S GGGACGCGGCGCTCGGTCAT/SQSN

FILE 'CAPLUS' ENTERED AT 15:43:15 ON 15 DEC 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 15 Dec 2005 VOL 143 ISS 25
FILE LAST UPDATED: 14 Dec 2005 (20051214/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply.

Searcher : Shears 571-272-2528

They are available for your review at:

http://www.cas.org/infopolicy.html

L2 23 S L1

L2 ANSWER 1 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 22 Jul 2005
ACCESSION NUMBER: 2005:635712 CAPLUS
DOCUMENT NUMBER: 143:113556
TITLE: Gene expression profiles and biomarkers for the detection of Alzheimer's disease-related and other disease-related gene transcripts in blood
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Ltd., Can.
SOURCE: U.S. Pat. Appl. Publ., 155 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2005079514	A1	20050414	US 2004-812827		20040330
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2004265869	A1	20041230	US 2004-812716		20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular Alzheimer's disease, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen.

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for detection of Alzheimer's disease-related and other disease-related gene transcripts in blood)

L2 ANSWER 2 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 14 Jul 2005
ACCESSION NUMBER: 2005:607198 CAPLUS
DOCUMENT NUMBER: 143:92045
TITLE: Gene expression profiling for diagnosis, prognosis, and therapy of osteoarthritis and other diseases using microarrays
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 157 pp., Cont.-in-part of U.S. Ser. No. 802,275.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2005123938	A1	20050609	US 2004-809675		20040325
US 2004037841	A1	20040226	US 2002-85783		20020228
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2005123938	A1	20050609	US 2004-809675		20040325
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2001-271955P	P	20010228
			US 2001-275017P	P	20010312
			US 2001-305340P	P	20010713
			US 2002-85783	A2	20020228
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312
			US 2004-809675	A	20040325

AB The present invention relates to gene expression profiling for diagnosis, prognosis and therapy of osteoarthritis and other diseases using microarray methods. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing and monitoring diseases

using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used todetect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention also describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiling for diagnosis, prognosis, and therapy of osteoarthritis and other diseases using microarrays)

L2 ANSWER 3 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 23 Mar 2005
ACCESSION NUMBER: 2005:248644 CAPLUS
DOCUMENT NUMBER: 142:274057
TITLE: Sequences of human schizophrenia related genes and use for diagnosis, prognosis and therapy
INVENTOR(S): Liew, Choong-chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 156 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004241727	A1	20041202	US 2004-812731		20040330
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2004241727	A1	20041202	US 2004-812731		20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312
			US 2004-812731	A	20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing and monitoring diseases using gene-specific and/or tissue-specific primers. The present invention also describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; sequences of human schizophrenia-related genes and use for diagnosis, prognosis and therapy)

L2 ANSWER 4 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 16 Mar 2005
ACCESSION NUMBER: 2005:228906 CAPLUS
DOCUMENT NUMBER: 142:292243
TITLE: The DNA sequence of the human X chromosome
AUTHOR(S): Ross, Mark T.; Grafham, Darren V.; Coffey, Alison J.; Scherer, Steven; McLay, Kirsten; Muzny, Donna; Platzer, Matthias; Howell, Gareth R.; Burrows, Christine; Bird, Christine P.; Frankish, Adam; Lovell, Frances L.; Howe, Kevin L.; Ashurst, Jennifer L.; Fulton, Robert S.; Sudbrak, Ralf; Wen, Gaiping; Jones, Matthew C.; Hurles, Matthew E.; Andrews, T. Daniel; Scott, Carol E.; Searle, Stephen; Ramser, Juliane; Whittaker, Adam; Deadman, Rebecca; Carter, Nigel P.; Hunt, Sarah E.; Chen, Rui; Cree, Andrew; Gunaratne, Preethi; Havlak, Paul; Hodgson, Anne; Metzker, Michael L.; Richards, Stephen; Scott, Graham; Steffen, David; Sodergren, Erica; Wheeler, David A.; Worley, Kim C.; Ainscough, Rachael; Ambrose, Kerrie D.; Ansari-Lari, M. Ali; Aradhya, Swaroop; Ashwell, Robert I. S.; Babbage, Anne K.; Bagguley, Claire L.; Ballabio, Andrea; Banerjee, Ruby; Barker, Gary E.; Barlow, Karen F.; Barrett, Ian P.; Bates, Karen N.; Beare, David M.; Beasley, Helen; Beasley, Oliver; Beck, Alfred; Bethel, Graeme; Blechschmidt, Karin; Brady, Nicola; Bray-Allen, Sarah; Bridgeman, Anne M.; Brown, Andrew J.; Brown, Mary J.; Bonnin, David; Bruford, Elspeth A.; Buhay, Christian; Burch, Paula; Burford, Deborah; Burgess, Joanne; Burrill, Wayne; Burton, John; Bye, Jackie M.; Carder, Carol; Carrel, Laura; Chako, Joseph; Chapman, Joanne C.; Chavez, Dean; Chen, Ellson; Chen, Guan; Chen, Yuan; Chen, Zhijian; Chinault, Craig; Ciccodicola, Alfredo; Clark, Sue Y.; Clarke, Graham; Clee, Chris M.; Clegg, Sheila; Clerc-Blankenburg, Kerstin; Clifford, Karen; Cobley, Vicky; Cole, Charlotte G.; Conquer, Jen S.; Corby, Nicole; Connor, Richard E.; David, Robert; Davies, Joy; Davis, Clay; Davis, John; Delgado, Oliver; DeShazo,

Denise; Dhami, Pawandeep; Ding, Yan; Dinh, Huyen; Dodsworth, Steve; Draper, Heather; Dugan-Rocha, Shannon; Dunham, Andrew; Dunn, Matthew; Durbin, K. James; Dutta, Ireena; Eades, Tamsin; Ellwood, Matthew; Emery-Cohen, Alexandra; Errington, Helen; Evans, Kathryn L.; Faulkner, Louisa; Francis, Fiona; Frankland, John; Fraser, Audrey E.; Galgoczy, Petra; Gilbert, James; Gill, Rachel; Gloeckner, Gernot; Gregory, Simon G.; Gribble, Susan; Griffiths, Coline; Grocock, Russell; Gu, Yanghong; Gwilliam, Rhian; Hamilton, Cerissa; Hart, Elizabeth A.; Hawes, Alicia; Heath, Paul D.; Heitmann, Katja; Hennig, Steffen; Hernandez, Judith; Hinzmann, Bernd; Ho, Sarah; Hoffs, Michael; Howden, Phillip J.; Huckle, Elizabeth J.; Hume, Jennifer; Hunt, Paul J.; Hunt, Adrienne R.; Isherwood, Judith; Jacob, Leni; Johnson, David; Jones, Sally; de Jong, Pieter J.; Joseph, Shirin S.; Keenan, Stephen; Kelly, Susan; Kershaw, Joanne K.; Khan, Ziad; Kioschis, Petra; Klages, Sven; Knights, Andrew J.; Kosiura, Anna; Kovar-Smith, Christie; Laird, Gavin K.; Langford, Cordelia; Lawlor, Stephanie; Leversha, Margaret; Lewis, Lora; Liu, Wen; Lloyd, Christine; Lloyd, David M.; Loulseged, Hermela; Loveland, Jane E.; Lovell, Jamieson D.; Lozado, Ryan; Lu, Jing; Lyne, Rachael; Ma, Jie; Maheshwari, Manjula; Matthews, Lucy H.; McDowall, Jennifer; McLaren, Stuart; McMurray, Amanda; Meidl, Patrick; Meitinger, Thomas; Milne, Sarah; Miner, George; Mistry, Shailesh L.; Morgan, Margaret; Morris, Sidney; Mueller, Ines; Mullikin, James C.; Nguyen, Ngoc; Nordsiek, Gabriele; Nyakatura, Gerald; O'Dell, Christopher N.; Okwuonu, Geoffery; Palmer, Sophie; Pandian, Richard; Parker, David; Parrish, Julia; Pasternak, Shiran; Patel, Dina; Pearce, Alex V.; Pearson, Danita M.; Pelan, Sarah E.; Perez, Lesette; Porter, Keith M.; Ramsey, Yvonne; Reichwald, Kathrin; Rhodes, Susan; Ridler, Kerry A.; Schlessinger, David; Schueler, Mary G.; Sehra, Harminder K.; Shaw-Smith, Charles; Shen, Hua; Sheridan, Elizabeth M.; Shownkeen, Ratna; Skuce, Carl D.; Smith, Michelle L.; Sotheran, Elizabeth C.; Steingruber, Helen E.; Steward, Charles A.; Storey, Roy; Swann, R. Mark; Swarbreck, David; Tabor, Paul E.; Taudien, Stefan; Taylor, Tineace; Teague, Brian; Thomas, Karen; Thorpe, Andrea; Timms, Kirsten; Tracey, Alan; Trevanion, Steve; Tromans, Anthony C.; d'Urso, Michele; Verduzco, Daniel; Villasana, Donna; Waldron, Lenee; Wall, Melanie; Wang, Qiaoyan; Warren, James; Warry, Georgina L.; Wei, Xuehong; West, Anthony; Whitehead, Siobhan L.; Whiteley, Mathew N.; Wilkinson, Jane E.; Willey, David L.; Williams, Gabrielle; Williams, Leanne; Williamson, Angela; Williamson, Helen; Wilming, Laurens; Woodmansey, Rebecca L.; Wray, Paul W.; Yen, Jennifer; Zhang, Jingkun; Zhou, Jianling; Zoghbi, Huda; Zorilla, Sara; Buck, David; Reinhardt, Richard; Poustka,

Annemarie; Rosenthal, Andre; Lehrach, Hans; Meindl, Alfons; Minx, Patrick J.; Hillier, LaDeana W.; Willard, Huntington F.; Wilson, Richard K.; Waterston, Robert H.; Rice, Catherine M.; Vaudin, Mark; Coulson, Alan; Nelson, David L.; Weinstock, George; Sulston, John E.; Durbin, Richard; Hubbard, Tim; Gibbs, Richard A.; Beck, Stephan; Rogers, Jane; Bentley, David R.

CORPORATE SOURCE: Wellcome Trust Genome Campus, The Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA, UK

SOURCE: Nature (London, United Kingdom) (2005), 434(7031), 325-337
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The human X chromosome has a unique biol. that was shaped by its evolution as the sex chromosome shared by males and females. This report provides 99.3% of the euchromatic sequence of the X chromosome. The anal. illustrates the autosomal origin of the mammalian sex chromosomes, the stepwise process that led to the progressive loss of recombination between X and Y, and the extent of subsequent degradation of the Y chromosome. LINE1 repeat elements cover one-third of the X chromosome, with a distribution that is consistent with their proposed role as way stations in the process of X-chromosome inactivation. There were 1098 genes found in the sequence, of which 99 encode proteins expressed in testis and in various tumor types. A disproportionately high number of Mendelian diseases are documented for the X chromosome. Of this number, 168 have been explained by mutations in 113 X-linked genes, which in many cases were characterized with the aid of the DNA sequence.

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; DNA sequence of the human X chromosome)

REFERENCE COUNT: 68 THERE ARE 68 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 02 Mar 2005

ACCESSION NUMBER: 2005:172213 CAPLUS

DOCUMENT NUMBER: 142:259426

TITLE: Gene expression profiles and biomarkers for the detection of asthma-related and other disease-related gene transcripts in blood

INVENTOR(S): Liew, Choong-Chin

PATENT ASSIGNEE(S): Chondrogene Limited, Can.

SOURCE: U.S. Pat. Appl. Publ., 156 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 47

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005042630	A1	20050224	US 2004-816357	20040401

US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2005042630	A1	20050224	US 2004-816357	20040401
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-816357	A 20040401

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular asthma, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of three records for this document necessitated by the large number of index entries required to fully index the docoment and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for the detection of asthma-related and other disease-related gene transcripts in blood)

L2 ANSWER 6 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 24 Feb 2005

ACCESSION NUMBER:	2005:156680 CAPLUS
DOCUMENT NUMBER:	142:238007
TITLE:	Gene expression profiles and biomarkers for the detection of hyperlipidemia and other disease-related gene transcripts in blood
INVENTOR(S):	Liew, Choong-Chin
PATENT ASSIGNEE(S):	Chondrogene Limited, Can.
SOURCE:	U.S. Pat. Appl. Publ., 155 pp., Cont.-in-part of U.S. Ser. No. 802,875. CODEN: USXXCO
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	47

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004248170	A1	20041209	US 2004-812777		20040330
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2004248170	A1	20041209	US 2004-812777		20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312
			US 2004-812777	A	20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular hyperlipidemia, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for detection of hyperlipidemia and other disease-related gene transcripts in blood)

L2 ANSWER 7 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 24 Feb 2005
ACCESSION NUMBER: 2005:155679 CAPLUS
DOCUMENT NUMBER: 142:213366
TITLE: Quantitative RT-PCR method for the detection in blood of microarray-identified rheumatoid arthritis-related gene transcripts for diagnosing and monitoring disease state
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.

SOURCE: U.S. Pat. Appl. Publ., 81 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005003394	A1	20050106	US 2004-812782	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2005003394	A1	20050106	US 2004-812782	20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-812782	A 20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood for diagnosing and monitoring diseases. The present invention demonstrates that a simple drop of blood may be used to determine the quant. expression of various mRNAs that reflect the health/disease state of the subject through the use of quant. reverse transcription-polymerase chain reaction (QRT-PCR) anal. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing and monitoring rheumatoid arthritis using gene-specific and/or tissue-specific primers. The present invention also describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; quant. RT-PCR method for the detection in blood of microarray-identified rheumatoid arthritis-related gene transcripts for diagnosing and monitoring disease state)

L2 ANSWER 8 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 18 Feb 2005
ACCESSION NUMBER: 2005:139371 CAPLUS
DOCUMENT NUMBER: 142:195820
TITLE: Gene expression profiles and biomarkers for the

detection of Chagas disease and other disease-related gene transcripts in blood

INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.

SOURCE: U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004241729	A1	20041202	US 2004-813097		20040330
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2004241729	A1	20041202	US 2004-813097		20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312
			US 2004-813097	A	20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular Chagas disease, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for the detection of Chagas disease and other disease-related gene transcripts in blood)

L2 ANSWER 9 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 18 Feb 2005
ACCESSION NUMBER: 2005:139369 CAPLUS
DOCUMENT NUMBER: 142:175392
TITLE: Analysis of genetic information contained in peripheral blood for diagnosis, prognosis and monitoring treatment of allergy, infection and genetic disease in human
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 155 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004241726	A1	20041202	US 2004-812707	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2004241726	A1	20041202	US 2004-812707	20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-812707	A 20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular allergy, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **261331-76-4**

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; anal. of genetic information contained in peripheral blood for diagnosis, prognosis and monitoring treatment of allergy, infection and genetic disease in human)

L2 ANSWER 10 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Feb 2005
ACCESSION NUMBER: 2005:112850 CAPLUS
DOCUMENT NUMBER: 142:153469
TITLE: Gene expression profiles and biomarkers for the detection of lung disease-related and other disease-related gene transcripts in blood
INVENTOR(S): Liew, Choong-chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 155 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004241728	A1	20041202	US 2004-812764	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2004241728	A1	20041202	US 2004-812764	20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-812764	A 20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing and monitoring diseases using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention also describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a

particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for the detection of lung disease-related and other disease-related gene transcripts in blood)

L2 ANSWER 11 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Feb 2005
ACCESSION NUMBER: 2005:112755 CAPLUS
DOCUMENT NUMBER: 142:153476
TITLE: Gene expression profiles and biomarkers for the detection of depression-related and other disease-related gene transcripts in blood
INVENTOR(S): Liew, Choong-chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004265868	A1	20041230	US 2004-812702		20040330
US 2004014059	A1	20040122	US 2002-268730		20021009
US 2005191637	A1	20050901	US 2004-803737		20040318
US 2005196762	A1	20050908	US 2004-803759		20040318
US 2005196763	A1	20050908	US 2004-803857		20040318
US 2005196764	A1	20050908	US 2004-803858		20040318
US 2005208505	A1	20050922	US 2004-803648		20040318
US 2004265868	A1	20041230	US 2004-812702		20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P	19990106
			US 2000-477148	B1	20000104
			US 2002-268730	A2	20021009
			US 2003-601518	A2	20030620
			US 2004-802875	A2	20040312
			US 2004-812702	A	20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular mental depression, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid

arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles and biomarkers for the detection of depression-related and other disease-related gene transcripts in blood)

L2 ANSWER 12 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 25 Jan 2005
ACCESSION NUMBER: 2005:65977 CAPLUS
DOCUMENT NUMBER: 142:128768
TITLE: Genetic polymorphisms in genes and their associated transcripts and encoded proteins associated with coronary stenosis and their use in diagnosis and drug screening
INVENTOR(S): Cargill, Michele; Devlin, James J.; Luke, May M.
PATENT ASSIGNEE(S): Applera Corporation, USA
SOURCE: PCT Int. Appl., 146 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 20
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004081186	A2	20040923	WO 2004-XB7140	20040310
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2004081186	A2	20040923	WO 2004-US7140	20040310
WO 2004081186	C1	20050120		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE,				

DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2003-453050P P 20030310

US 2003-466437P P 20030430

WO 2004-US7140 A 20040310

AB The present invention is based on the discovery of genetic polymorphisms that are associated with coronary artery stenosis. In particular, the present invention relates to nucleic acid mols. containing the polymorphisms, variant proteins encoded by such nucleic acid mols., reagents for detecting the polymorphic nucleic acid mols. and proteins, and methods of using the nucleic acid and proteins as well as methods of using reagents for their detection. The present invention provides 697 transcript sequences, 697 encoded protein sequences, 443 genomic sequences, 10,766 transcript-based context sequences for polymorphisms, 55,168 genomic-based context sequences for polymorphisms, and 762 primer sequences. [This abstract record is one of 14 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **823929-82-4**
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; genetic polymorphisms in genes and their associated transcripts and encoded proteins associated with coronary stenosis and their use in diagnosis and drug screening)

L2 ANSWER 13 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 05 Aug 2004
ACCESSION NUMBER: 2004:627106 CAPLUS
DOCUMENT NUMBER: 141:117899
TITLE: Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
AUTHOR(S): Fu, Glenn K.; Wang, Jonathan T.; Yang, Junming; Au-Young, Janice; Stuve, Laura L.
CORPORATE SOURCE: Incyte Corporation, Palo Alto, CA, 94304, USA
SOURCE: Genomics (2004), 84(1), 205-210
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The rapid amplification of cDNA ends (RACE) procedure is a widely used PCR-based method to clone the cDNA ends of mRNA transcripts. Current RACE methods often produce a high background of nonspecific PCR products, which can exclude the identification of the target cDNA of interest. An improved RACE procedure is described which uses circular cDNA templates, and the successful extension cloning of 4406 cDNAs is demonstrated. The cRACE extension clone sequences are deposited in GenBank/DDBJ/EMBL with accession nos. CD607123-CD638268. [This abstract record is one of eight records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **632444-15-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes)

L2 ANSWER 14 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 15 Apr 2004
ACCESSION NUMBER: 2004:306379 CAPLUS
DOCUMENT NUMBER: 140:332466
TITLE: Compositions and methods for treatment of prostate and other cancers
INVENTOR(S): Gleave, Martin E.; Rocchi, Palma; Signaevsky, Maxim
PATENT ASSIGNEE(S): The University of British Columbia, Can.
SOURCE: PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2004030660	A2	20040415	WO 2003-CA1588		20031002
WO 2004030660	A3	20040610			
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG					
CA 2498026	AA	20040415	CA 2003-2498026		20031002
US 2004127441	A1	20040701	US 2003-605498		20031002
EP 1545561	A2	20050629	EP 2003-769111		20031002
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK					
NO 2005002055	A	20050623	NO 2005-2055		20050427
PRIORITY APPLN. INFO.:			US 2002-415859P	P	20021002
			US 2003-463952P	P	20030418
			WO 2003-CA1588	W	20031002

AB The present invention makes use of therapeutic agents which target heat shock protein (hsp) 27 in vivo to provide treatment to individuals, particularly human individuals, suffering from prostate cancer and other cancers that overexpress hsp 27. In accordance with the invention, a therapeutic agent, for example an antisense oligonucleotide or RNAi nucleotide inhibitor with sequence specificity for hsp 27 mRNA, for example human hsp 27 mRNA, is administered to an indvididvual suffering from prostate cancer or some other cancer expressing elevated levels of hsp 27 in a therapeutically effective amount The therapeutic agent is suitably formulated into a pharmaceutical composition which includes a pharmaceutically acceptable carrier, and packaged in dosage unit form. A preferred dosage unit

form is in injectable dosage unit form.
IT **679855-00-6 679855-01-7**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(oligonucleotide methods for treatment of prostate and other cancers overexpressing hsp27)

L2 ANSWER 15 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Apr 2004
ACCESSION NUMBER: 2004:290693 CAPLUS
DOCUMENT NUMBER: 140:282210
TITLE: Numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection
AUTHOR(S): Porcel, Betina M.; Delfour, Olivier; Castelli, Vanina; De Berardinis, Veronique; Friedlander, Lucie; Cruaud, Corinne; Ureta-Vidal, Abel; Scarpelli, Claude; Wincker, Patrick; Schaechter, Vincent; Saurin, William; Gyapay, Gabor; Salanoubat, Marcel; Weissenbach, Jean
CORPORATE SOURCE: Genoscope-Centre National de Sequencage and CNRS UMR-8030, Evry, 91000, Fr.
SOURCE: Genome Research (2004), 14(3), 463-471
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A collection of 90,000 human cDNA clones generated to increase the fraction of "full-length" cDNAs available was analyzed by sequence alignment on the human genome assembly. Five hundred fifty-two gene models not found in LocusLink, with coding regions of ≥300 bp, were defined by using this collection. Exon composition proposed for novel genes showed an average of 4.7 exons per gene. In 20% of the cases, at least half of the exons predicted for new genes coincided with evolutionary conserved regions defined by sequence comparisons with the pufferfish Tetraodon nigroviridis. Among this subset, CpG islands were observed at the 5' end of 75%. In-frame stop codons upstream of the initiator ATG were present in 49% of the new genes, and 16% contained a coding region comprising at least 50% of the cDNA sequence. This cDNA resource also provided candidate small protein-coding genes, usually not included in genome annotations. In addition, anal. of a sample from this cDNA collection indicates that .apprx.380 gene models described in LocusLink could be extended at their 5' end by at least one new exon. Finally, this cDNA resource provided an exptl. support for annotations based exclusively on predictions, thus representing a resource substantially improving the human genome annotation. [This abstract record is one of 53 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **323106-08-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection)

L2 ANSWER 16 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Apr 2004
ACCESSION NUMBER: 2004:290692 CAPLUS
DOCUMENT NUMBER: 140:265377

TITLE: Numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection

AUTHOR(S): Porcel, Betina M.; Delfour, Olivier; Castelli, Vanina; De Berardinis, Veronique; Friedlander, Lucie; Cruaud, Corinne; Ureta-Vidal, Abel; Scarpelli, Claude; Wincker, Patrick; Schaechter, Vincent; Saurin, William; Gyapay, Gabor; Salanoubat, Marcel; Weissenbach, Jean

CORPORATE SOURCE: Genoscope-Centre National de Sequencage and CNRS UMR-8030, Evry, 91000, Fr.

SOURCE: Genome Research (2004), 14(3), 463-471
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A collection of 90,000 human cDNA clones generated to increase the fraction of "full-length" cDNAs available was analyzed by sequence alignment on the human genome assembly. Five hundred fifty-two gene models not found in LocusLink, with coding regions of ≥300 bp, were defined by using this collection. Exon composition proposed for novel genes showed an average of 4.7 exons per gene. In 20% of the cases, at least half of the exons predicted for new genes coincided with evolutionary conserved regions defined by sequence comparisons with the pufferfish Tetraodon nigroviridis. Among this subset, CpG islands were observed at the 5' end of 75%. In-frame stop codons upstream of the initiator ATG were present in 49% of the new genes, and 16% contained a coding region comprising at least 50% of the cDNA sequence. This cDNA resource also provided candidate small protein-coding genes, usually not included in genome annotations. In addition, anal. of a sample from this cDNA collection indicates that .apprx.380 gene models described in LocusLink could be extended at their 5' end by at least one new exon. Finally, this cDNA resource provided an exptl. support for annotations based exclusively on predictions, thus representing a resource substantially improving the human genome annotation. [This abstract record is one of 53 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **323065-65-2 323094-05-9**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection)

L2 ANSWER 17 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN

ED Entered STN: 09 Apr 2004

ACCESSION NUMBER: 2004:290690 CAPLUS

DOCUMENT NUMBER: 140:265376

TITLE: Numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection

AUTHOR(S): Porcel, Betina M.; Delfour, Olivier; Castelli, Vanina; De Berardinis, Veronique; Friedlander, Lucie; Cruaud, Corinne; Ureta-Vidal, Abel; Scarpelli, Claude; Wincker, Patrick; Schaechter, Vincent; Saurin, William; Gyapay, Gabor; Salanoubat, Marcel; Weissenbach, Jean

CORPORATE SOURCE: Genoscope-Centre National de Sequencage and CNRS UMR-8030, Evry, 91000, Fr.

SOURCE: Genome Research (2004), 14(3), 463-471
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A collection of 90,000 human cDNA clones generated to increase the fraction of "full-length" cDNAs available was analyzed by sequence alignment on the human genome assembly. Five hundred fifty-two gene models not found in LocusLink, with coding regions of ≥300 bp, were defined by using this collection. Exon composition proposed for novel genes showed an average of 4.7 exons per gene. In 20% of the cases, at least half of the exons predicted for new genes coincided with evolutionary conserved regions defined by sequence comparisons with the pufferfish Tetraodon nigroviridis. Among this subset, CpG islands were observed at the 5' end of 75%. In-frame stop codons upstream of the initiator ATG were present in 49% of the new genes, and 16% contained a coding region comprising at least 50% of the cDNA sequence. This cDNA resource also provided candidate small protein-coding genes, usually not included in genome annotations. In addition, anal. of a sample from this cDNA collection indicates that .apprx.380 gene models described in LocusLink could be extended at their 5' end by at least one new exon. Finally, this cDNA resource provided an exptl. support for annotations based exclusively on predictions, thus representing a resource substantially improving the human genome annotation. [This abstract record is one of 53 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **323020-46-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection)

L2 ANSWER 18 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 09 Apr 2004
ACCESSION NUMBER: 2004:290686 CAPLUS
DOCUMENT NUMBER: 140:265374
TITLE: Numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection
AUTHOR(S): Porcel, Betina M.; Delfour, Olivier; Castelli, Vanina; De Berardinis, Veronique; Friedlander, Lucie; Cruaud, Corinne; Ureta-Vidal, Abel; Scarpelli, Claude; Wincker, Patrick; Schaechter, Vincent; Saurin, William; Gyapay, Gabor; Salanoubat, Marcel; Weissenbach, Jean
CORPORATE SOURCE: Genoscope-Centre National de Sequencage and CNRS UMR-8030, Evry, 91000, Fr.
SOURCE: Genome Research (2004), 14(3), 463-471
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A collection of 90,000 human cDNA clones generated to increase the fraction of "full-length" cDNAs available was analyzed by sequence alignment on the human genome assembly. Five hundred fifty-two gene models not found in LocusLink, with coding regions of ≥300 bp, were defined by using this collection. Exon composition proposed for novel genes showed an average of 4.7 exons per gene. In 20% of the cases, at

least half of the exons predicted for new genes coincided with evolutionary conserved regions defined by sequence comparisons with the pufferfish Tetraodon nigroviridis. Among this subset, CpG islands were observed at the 5' end of 75%. In-frame stop codons upstream of the initiator ATG were present in 49% of the new genes, and 16% contained a coding region comprising at least 50% of the cDNA sequence. This cDNA resource also provided candidate small protein-coding genes, usually not included in genome annotations. In addition, anal. of a sample from this cDNA collection indicates that .apprx.380 gene models described in LocusLink could be extended at their 5' end by at least one new exon. Finally, this cDNA resource provided an exptl. support for annotations based exclusively on predictions, thus representing a resource substantially improving the human genome annotation. [This abstract record is one of 53 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **322035-57-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; numerous novel annotations of the human genome sequence supported by a 5'-end-enriched cDNA collection)

L2 ANSWER 19 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 03 Feb 2004
ACCESSION NUMBER: 2004:85983 CAPLUS
DOCUMENT NUMBER: 140:194431
TITLE: Human prostate cancer marker genes associated with various metastatic stages identified by gene profiling, and related compositions, kits, and methods for diagnosis, prognosis and therapy
INVENTOR(S): Schlegel, Robert; Endege, Wilson O.
PATENT ASSIGNEE(S): Millennium Pharmaceuticals, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 131 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2004009481	A1	20040115	US 2002-166883		20020611
US 2004009481	A1	20040115	US 2002-166883		20020611
PRIORITY APPLN. INFO.:			US 2001-297285P	P	20010611
			US 2002-166883	A	20020611

AB The invention relates to compns., kits, and methods for diagnosing, staging, prognosing, monitoring and treating human prostate cancers. A variety of marker genes are provided, wherein changes in the levels of expression of one or more of the marker genes is correlated with the presence of prostate cancer. In particular, three sets of the marker genes, corresponding to 11617 GenBank Accession Nos. (only 2168 new submissions) and 15 SEQ IDs, are identified by transcription profiling using RNA derived from clin. samples, that were expressed at least 2-fold or greater than the normal controls. Using TNM staging approach, these markers are divided to three groups, ones can be used to determine whether prostate cancer has metastasized, or is likely to metastasize, to the liver (M stage); ones can be used to determine whether

prostate cancer has metastasized, or is likely to metastasize, to the bone (M stage); and ones can be used to determine whether prostate cancer has metastasized, or is likely to metastasize, to the lymph nodes (N stage and/or M stage). The invention also relates to a kit for assessing the specific type of metastatic prostate cancer, e.g., cancer that has metastasized to the liver, bone or lymph nodes. [This abstract record is one of three records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **224874-53-7 261331-76-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; human prostate cancer marker genes associated with various metastatic stages identified by gene profiling, and related compns., kits, and methods for diagnosis, prognosis and therapy)

L2 ANSWER 20 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 10 Jul 2003
ACCESSION NUMBER: 2003:524770 CAPLUS
DOCUMENT NUMBER: 139:128820
TITLE: The DNA sequence of human chromosome 7
AUTHOR(S): Hillier, LaDeana W.; Fulton, Robert S.; Fulton, Lucinda A.; Graves, Tina A.; Pepin, Kymberlie H.; Wagner-McPherson, Caryn; Layman, Dan; Maas, Jason; Jaeger, Sara; Walker, Rebecca; Wylie, Kristine; Sekhon, Mandeep; Becker, Michael C.; O'Laughlin, Michelle D.; Schaller, Mark E.; Fewell, Ginger A.; Delehaunty, Kimberly D.; Miner, Tracie L.; Nash, William E.; Cordes, Matt; Du, Hui; Sun, Hui; Edwards, Jennifer; Bradshaw-Cordum, Holland; Ali, Johar; Andrews, Stephanie; Isak, Amber; VanBrunt, Andrew; Nguyen, Christine; Du, Feiyu; Lamar, Betty; Courtney, Laura; Kalicki, Joelle; Ozersky, Philip; Bielicki, Lauren; Scott, Kelsi; Holmes, Andrea; Harkins, Richard; Harris, Anthony; Strong, Cynthia Madsen; Hou, Shunfang; Tomlinson, Chad; Dauphin-Kohlberg, Sara; Kozlowicz-Reilly, Amy; Leonard, Shawn; Rohlfing, Theresa; Rock, Susan M.; Tin-Wollam, Aye-Mon; Abbott, Amanda; Minx, Patrick; Maupin, Rachel; Strowmatt, Catrina; Latreille, Phil; Miller, Nancy; Johnson, Doug; Murray, Jennifer; Woessner, Jeffrey P.; Wendl, Michael C.; Yang, Shiaw-Pyng; Schultz, Brian R.; Wallis, John W.; Spieth, John; Bieri, Tamberlyn A.; Nelson, Joanne O.; Berkowicz, Nicolas; Wohldmann, Patricia E.; Cook, Lisa L.; Hickenbotham, Matthew T.; Eldred, James; Williams, Donald; Bedell, Joseph A.; Mardis, Elaine R.; Clifton, Sandra W.; Chissoe, Stephanie L.; Marra, Marco A.; Raymond, Christopher; Haugen, Eric; Gillett, Will; Zhou, Yang; James, Rose; Phelps, Karen; Iadanoto, Shawn; Bubb, Kerry; Simms, Elizabeth; Levy, Ruth; Clendenning, James; Kaul, Rajinder; Kent, W. James; Furey, Terrence S.; Baertsch, Robert A.; Brent, Michael R.; Keibler, Evan; Flicek, Paul; Bork, Peer; Suyama, Mikita; Bailey, Jeffrey A.; Portnoy, Matthew E.; Torrents, David; Chinwalla, Asif T.; Gish, Warren R.; Eddy,

Sean R.; McPherson, John D.; Olson, Maynard V.; Eichler, Evan E.; Green, Eric D.; Waterston, Robert H.; Wilson, Richard K.
CORPORATE SOURCE: Genome Sequencing Center, Washington University School of Medicine, St Louis, MO, 63108, USA
SOURCE: Nature (London, United Kingdom) (2003), 424(6945), 157-164
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Human chromosome 7 has historically received prominent attention in the human genetics community, primarily related to the search for the cystic fibrosis gene and the frequent cytogenetic changes associated with various forms of cancer. More than 153 million base pairs are presented, representing 99.4% of the euchromatic sequence of chromosome 7, the first metacentric chromosome completed so far. The sequence has excellent concordance with previously established phys. and genetic maps, and it exhibits an unusual amount of segmentally duplicated sequence (8.2%), with marked differences between the two arms. Initial analyses have identified 1150 protein-coding genes, 605 of which were confirmed by cDNA sequences, and an addnl. 941 pseudogenes. Of genes confirmed by transcript sequences, some are polymorphic for mutations that disrupt the reading frame.
IT **224874-53-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; DNA sequence of human chromosome 7)
REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 21 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Jan 2003
ACCESSION NUMBER: 2003:24612 CAPLUS
DOCUMENT NUMBER: 138:50950
TITLE: Gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators of ovarian cancer
INVENTOR(S): Mack, David H.; Gish, Kurt C.
PATENT ASSIGNEE(S): Eos Biotechnology Inc., USA
SOURCE: PCT Int. Appl., 332 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 38
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002102235	A2	20021227	WO 2002-XC19297	20020618

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,

CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

US 2004005563	A1	20040108	US 2002-173999	20020617
WO 2002102235	A2	20021227	WO 2002-US19297	20020618
WO 2002102235	A3	20050203		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
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SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

US 2003124579	A1	20030703	US 2002-235399	20020904
US 2004197325	A1	20041007	US 2003-741657	20031219

PRIORITY APPLN. INFO.:	US 2001-299234P	P	20010618
	US 2001-315287P	P	20010827
	US 2001-317544P	P	20010905
	US 2001-350666P	P	20011113
	US 2002-372246P	P	20020412
	WO 2002-US19297	W	20020618
	US 2002-173999	A	20020617
	US 2002-435618P	P	20021220

AB Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer compared to normal adult tissues. The genes are identified using the Affymetrix/Eos Hu01 or Hu03 GeneChip microarrays containing 35,403 and 59,680 probesets, resp. Related methods and compns. that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: ANT (Analyte); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators of ovarian cancer)

L2 ANSWER 22 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 13 Jan 2003
ACCESSION NUMBER: 2003:24609 CAPLUS
DOCUMENT NUMBER: 138:50948
TITLE: Gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators

of ovarian cancer
INVENTOR(S): Mack, David H.; Gish, Kurt C.
PATENT ASSIGNEE(S): Eos Biotechnology Inc., USA
SOURCE: PCT Int. Appl., 332 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 38
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002102235	A2	20021227	WO 2002-XA19297	20020618
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004005563	A1	20040108	US 2002-173999	20020617
WO 2002102235	A2	20021227	WO 2002-US19297	20020618
WO 2002102235	A3	20050203		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003124579	A1	20030703	US 2002-235399	20020904
US 2004197325	A1	20041007	US 2003-741657	20031219

PRIORITY APPLN. INFO.:			
US 2001-299234P	P	20010618	
US 2001-315287P	P	20010827	
US 2001-317544P	P	20010905	
US 2001-350666P	P	20011113	
US 2002-372246P	P	20020412	
WO 2002-US19297	W	20020618	
US 2002-173999	A	20020617	
US 2002-435618P	P	20021220	

AB Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer compared to normal adult tissues. The genes are identified using the Affymetrix/Eos Hu01 or Hu03

GeneChip microarrays containing 35,403 and 59,680 probesets, resp. Related methods and compns. that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: ANT (Analyte); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators of ovarian cancer)

L2 ANSWER 23 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 29 Dec 2002
ACCESSION NUMBER: 2002:977583 CAPLUS
DOCUMENT NUMBER: 138:34234
TITLE: Gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators of ovarian cancer
INVENTOR(S): Mack, David H.; Gish, Kurt C.
PATENT ASSIGNEE(S): Eos Biotechnology Inc., USA
SOURCE: PCT Int. Appl., 332 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 38
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002102235	A2	20021227	WO 2002-US19297	20020618
WO 2002102235	A3	20050203		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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US 2004005563	A1	20040108	US 2002-173999	20020617
CA 2451465	AA	20021227	CA 2002-2451465	20020618
WO 2002102235	A2	20021227	WO 2002-XA19297	20020618
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SN, TD, TG

WO 2002102235	A2	20021227	WO 2002-XB19297 20020618

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

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WO 2002102235	A2	20021227	WO 2002-XC19297 20020618

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2002102235	A2	20021227	WO 2002-XD19297 20020618

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1517998	A2	20050330	EP 2002-752063 20020618

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, LT, LV, FI, MK, CY, AL, TR

JP 2005508144	T2	20050331	JP 2003-504826 20020618
US 2003124579	A1	20030703	US 2002-235399 20020904
US 2004197325	A1	20041007	US 2003-741657 20031219

PRIORITY APPLN. INFO.:

US 2001-299234P	P	20010618
US 2001-315287P	P	20010827
US 2001-317544P	P	20010905
US 2001-350666P	P	20011113
US 2002-372246P	P	20020412
US 2002-173999	A	20020617
WO 2002-US19297	W	20020618
US 2002-435618P	P	20021220

Searcher : Shears 571-272-2528

AB Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer compared to normal adult tissues. The genes are identified using the Affymetrix/Eos Hu01 or Hu03 GeneChip microarrays containing 35,403 and 59,680 probesets, resp. Related methods and compns. that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **261331-76-4**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene expression profiles useful for diagnosis of human ovarian cancer and screening for modulators of ovarian cancer)

E1 THROUGH E11 ASSIGNED

FILE 'REGISTRY' ENTERED AT 15:43:53 ON 15 DEC 2005
L3 11 SEA FILE=REGISTRY ABB=ON PLU=ON (261331-76-4/BI OR 224874-53-7/BI OR 322035-57-4/BI OR 323020-46-8/BI OR 323065-65-2/BI OR 323094-05-9/BI OR 323106-08-7/BI OR 632444-15-6/BI OR 679855-00-6/BI OR 679855-01-7/BI OR 823929-82-4/BI)

L4 11 L1 AND L3

L4 ANSWER 1 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **823929-82-4** REGISTRY
CN DNA (human clone WO2004081186-SEQID-12491 coronary stenosis-associated protein gene plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1311: PN: WO2004081186 SEQID: 12491 claimed DNA
SQL 32086
MF Unspecified
CI MAN

REFERENCE 1: 142:128768

L4 ANSWER 2 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **679855-01-7** REGISTRY
CN DNA, d(G-G-G-A-C-G-C-G-G-C-G-C-T-C-G-G-T-C-A-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 82: PN: WO2004030660 SEQID: 82 claimed DNA
SQL 20
MF Unspecified
CI MAN

REFERENCE 1: 140:332466

L4 ANSWER 3 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **679855-00-6** REGISTRY
CN DNA, d(G-G-G-G-A-C-G-C-G-G-C-G-C-T-C-G-G-T-C-A-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 81: PN: WO2004030660 SEQID: 81 claimed DNA
SQL 21

MF Unspecified
CI MAN

REFERENCE 1: 140:332466

L4 ANSWER 4 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **632444-15-6** REGISTRY
CN DNA (human clone 56098972H1 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CD611948
SQL 696
MF Unspecified
CI MAN

REFERENCE 1: 141:117899

L4 ANSWER 5 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **323106-08-7** REGISTRY
CN DNA (human clone CS0DI068YA24 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL552709
SQL 725
MF Unspecified
CI MAN

REFERENCE 1: 140:282210

L4 ANSWER 6 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **323094-05-9** REGISTRY
CN DNA (human clone CS0DI063YO09 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL551506
SQL 715
MF Unspecified
CI MAN

REFERENCE 1: 140:265377

L4 ANSWER 7 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **323065-65-2** REGISTRY
CN DNA (human clone CS0DI036YH02 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL548665
SQL 785
MF Unspecified
CI MAN

REFERENCE 1: 140:265377

L4 ANSWER 8 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **323020-46-8** REGISTRY
CN DNA (human clone CS0DI020YI18 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL544146

SQL 753
MF Unspecified
CI MAN

REFERENCE 1: 140:265376

L4 ANSWER 9 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **322035-57-4** REGISTRY
CN DNA (human clone CS0DF006YN18 EST (expressed sequence tag)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL534829
SQL 810
MF Unspecified
CI MAN

REFERENCE 1: 140:265374

L4 ANSWER 10 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **261331-76-4** REGISTRY
CN DNA (human gene CACNA1F plus gene JM1 plus gene JM2 plus gene Hb2E) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2162: PN: US20050003394 TABLE: 3V unclaimed DNA
CN 2170: PN: US20040241726 TABLE: 3V unclaimed DNA
CN 2253: PN: US20040241728 TABLE: 3V unclaimed DNA
CN 2276: PN: US20040248170 TABLE: 3V unclaimed DNA
CN 2304: PN: US20050123938 TABLE: 3V unclaimed DNA
CN 2319: PN: US20050042630 TABLE: 3V unclaimed DNA
CN 2322: PN: US20040265868 TABLE: 3V unclaimed DNA
CN 2401: PN: US20040241729 TABLE: 3V unclaimed DNA
CN 2504: PN: US20040241727 TABLE: 3V unclaimed DNA
CN 4493: PN: US20050079514 TABLE: 3V unclaimed DNA
CN 4585: PN: US20040009481 TABLE: 1 claimed DNA
CN DNA (human clone multiple clones)
CN GenBank AF235097
SQL 140335
MF Unspecified
CI MAN

REFERENCE 1: 143:113556

REFERENCE 2: 143:92045

REFERENCE 3: 142:292243

REFERENCE 4: 142:274057

REFERENCE 5: 142:259426

REFERENCE 6: 142:238007

REFERENCE 7: 142:213366

REFERENCE 8: 142:195820

REFERENCE 9: 142:175392

REFERENCE 10: 142:153476

L4 ANSWER 11 OF 11 REGISTRY COPYRIGHT 2005 ACS on STN
RN **224874-53-7** REGISTRY
CN DNA (human clone CTA-363M4 chromosome 7 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3687: PN: US20040009481 TABLE: 1 claimed DNA
CN DNA (human clone CTA-363M4)
CN GenBank AC006388
SQL 59241
MF Unspecified
CI MAN

REFERENCE 1: 140:194431

REFERENCE 2: 139:128820

FILE 'MEDLINE' ENTERED AT 15:46:32 ON 15 DEC 2005

FILE 'BIOSIS' ENTERED AT 15:46:32 ON 15 DEC 2005

FILE 'EMBASE' ENTERED AT 15:46:32 ON 15 DEC 2005

FILE 'CANCERLIT' ENTERED AT 15:46:32 ON 15 DEC 2005

L6 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2001:47942 BIOSIS
DOCUMENT NUMBER: PREV200100047942
TITLE: JM2, encoding a fork head-related protein, is mutated in X-linked autoimmunity-allergic disregulation syndrome.
AUTHOR(S): Chatila, Talal A. [Reprint author]; Blaeser, Frank; Ho, Nga; Lederman, Howard M.; Voulgaropoulos, Constantine; Helms, Cindy; Bowcock, Anne M.
CORPORATE SOURCE: Division of Immunology/Rheumatology, Department of Pediatrics, Washington University School of Medicine, 660 S. Euclid Avenue, St. Louis, MO, 63110, USA chatila@kids.wustl.edu
SOURCE: Journal of Clinical Investigation, (December, 2000) Vol. 106, No. 12, pp. R75-R81. print. CODEN: JCINAO. ISSN: 0021-9738.
DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: Genbank-AF235097
ENTRY DATE: Entered STN: 24 Jan 2001
Last Updated on STN: 15 Feb 2002
AB X-linked autoimmunity-allergic disregulation syndrome (XLAAD) is an X-linked recessive immunological disorder characterized by multisystem autoimmunity, particularly early-onset type 1 diabetes mellitus, associated with manifestations of severe atopy including eczema, food allergy, and eosinophilic inflammation. Consistent with the allergic phenotype, analysis of two kindreds with XLAAD revealed marked skewing of patient T lymphocytes toward the Th2 phenotype. Using a positional-candidate approach, we have identified in both kindreds mutations in JM2, a gene on Xp11.23 that encodes a fork head domain-containing protein. One point mutation at a splice junction

site results in transcripts that encode a truncated protein lacking the fork head homology domain. The other mutation involves an in-frame, 3-bp deletion that is predicted to impair the function of a leucine zipper dimerization domain. Our results point to a critical role for JM2 in self tolerance and Th cell differentiation.

FILE 'HOME' ENTERED AT 15:46:32 ON 15 DEC 2005

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=> d his ful

     (FILE 'HOME' ENTERED AT 15:41:52 ON 15 DEC 2005)
               SET COST OFF

     FILE 'REGISTRY' ENTERED AT 15:41:59 ON 15 DEC 2005
L1             29 SEA ABB=ON  PLU=ON  GGGACGCGGCGCTCGGTCAT/SQSN

     FILE 'CAPLUS' ENTERED AT 15:42:50 ON 15 DEC 2005
L2             23 SEA ABB=ON  PLU=ON  L1

     FILE 'REGISTRY' ENTERED AT 15:43:15 ON 15 DEC 2005

     FILE 'CAPLUS' ENTERED AT 15:43:15 ON 15 DEC 2005
               D L2 1-23 .BEVSTR
               SEL HIT L2 1-23 RN

     FILE 'REGISTRY' ENTERED AT 15:43:53 ON 15 DEC 2005
L3             11 SEA ABB=ON  PLU=ON  (261331-76-4/BI OR 224874-53-7/BI OR
                  322035-57-4/BI OR 323020-46-8/BI OR 323065-65-2/BI OR
                  323094-05-9/BI OR 323106-08-7/BI OR 632444-15-6/BI OR
                  679855-00-6/BI OR 679855-01-7/BI OR 823929-82-4/BI)
                  D QUE
L4             11 SEA ABB=ON  PLU=ON  L1 AND L3
                  D L3 1-11 .BEVREG1

     FILE 'MEDLINE, BIOSIS, EMBASE, CANCERLIT' ENTERED AT 15:44:46 ON 15
     DEC 2005
L5              1 SEA ABB=ON  PLU=ON  L3

     FILE 'MEDLINE, BIOSIS, EMBASE, CANCERLIT' ENTERED AT 15:45:46 ON 15
     DEC 2005
L6              1 SEA ABB=ON  PLU=ON  L3

     FILE 'REGISTRY' ENTERED AT 15:46:30 ON 15 DEC 2005
               D L4 1-11 .BEVREG

     FILE 'MEDLINE, BIOSIS, EMBASE, CANCERLIT' ENTERED AT 15:46:32 ON 15
     DEC 2005
               D L6
               D L6 IBIB ABS

     FILE 'HOME' ENTERED AT 15:46:32 ON 15 DEC 2005


     FILE HOME

     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:   14 DEC 2005  HIGHEST RN 869939-98-0
     DICTIONARY FILE UPDATES:  14 DEC 2005  HIGHEST RN 869939-98-0

     New CAS Information Use Policies, enter HELP USAGETERMS for details.

     TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

       Please note that search-term pricing does apply when
```

conducting SmartSELECT searches.

```
**********************************************************************
*                                                                    *
* The CA roles and document type information have been removed from  *
* the IDE default display format and the ED field has been added,    *
* effective March 20, 2005.  A new display format, IDERL, is now     *
* available and contains the CA role and document type information.  *
*                                                                    *
**********************************************************************
```

Structure search iteration limits have been increased. See HELP SLIMI for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

FILE CAPLUS

FILE COVERS 1907 - 15 Dec 2005 VOL 143 ISS 25
FILE LAST UPDATED: 14 Dec 2005 (20051214/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply They are available for your review at:

http://www.cas.org/infopolicy.html

FILE MEDLINE
FILE LAST UPDATED: 8 DEC 2005 (20051208/UP). FILE COVERS 1950 TO DAT

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details on the 2005 reload, enter HELP RLOAD at an arrow promt (=>).
See also:

http://www.nlm.nih.gov/mesh/
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.ht
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

Searcher : Shears 571-272-2528

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE BIOSIS
FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 14 December 2005 (20051214/ED)

FILE EMBASE
FILE COVERS 1974 TO 8 Dec 2005 (20051208/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE CANCERLIT
FILE COVERS 1963 TO 15 Nov 2002 (20021115/ED)

On July 28, 2002, CANCERLIT was reloaded. See HELP RLOAD for details

CANCERLIT thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

This file contains CAS Registry Numbers for easy and accurate substan identification.